REMARKS

Restriction has been required between what the PTO deems to be four patentably distinct inventions, namely:

Group I, comprising claims 1-7 and 20 and drawn to a polypeptide capable of modulating the autoimmune response of an individual to acetylcholine receptor and pharmaceutical compositions comprising the same;

Group II, comprising claims 8-19 drawn to a method of producing a polypeptide comprising a DNA molecule, vectors, and cells comprising the same; and

Group III, comprising claim 21 and drawn to a method for alleviating and/or treating myasthenia gravis; and

Group IV, comprising claim 22 and drawn to a method for diagnosing myasthenia gravis.

Applicants elect Group II comprising claims 8-19 for prosecution on the merits.

The examiner further requires restriction to one of the sequences SEQ ID NOs:1, 2, 5, 6, 7 and 8.

Applicants provisionally elect SEQ ID NO:2, that is a DNA molecule encoding a polypeptide of SEQ ID NO:2, with traverse.

The reason for traversal is that SEQ ID NOs:1, 5, and 7 are nucleotide sequences which encode the amino acid

sequences SEQ ID NOs: 2, 6, and 8, respectively. Therefore, at least SEQ ID NO:1 which encodes for the amino acid sequence SEO ID NO:2 should be examined together with SEQ ID NO:2. Furthermore, as disclosed on pages 8 and 9 of the specification, the sequence are structurally and functionally similar. For example, SEQ ID NO:2 is residues 1-210 of the human acetylcholine receptor (hAChR) α -subunit, SEQ ID NO:6 is residues 1-210 of hAChR α -subunit but with a sequence of 25 residues encoded by the p3A exon of hAChR α -subunit inserted between residues 58 and 59, and SEQ ID NO:8 is residues 1-205 of hAChR α -subunit but with a sequence of 25 residues encoded by the p3A exon of hAChR α -subunit inserted between residues 58 and 59. Thus, the only difference between SEQ ID NO:6 and SEQ ID NO:8 is an extra five residues at the C-terminal end of SEQ ID NO:8 and the only difference between SEQ ID NO:2 and SEQ ID NO:6 is the 25 residue insertion between residues 58 and 59.

As the nucleotide sequences SEQ ID NOs:1, 5 and 7 encode amino acid sequences SEQ ID NOs:2, 6 and 8, they are also structurally and functionally related. Accordingly, each sequence does not require a separate search of the literature.

Withdrawal of the restriction requirement with regard to SEQ ID NOs:1, 2, 5, 6, 7 and 8 and examination of all SEQ ID NOs:1, 2, 5, 6, 7 and 8 are therefore respectfully requested.

In re of Appln. 00. 09/820,339

Attached hereto is a marked-up version of the changes made to the specification and claims by the current amendment. The attached page is captioned "Version with markings to show changes made".

Respectfully submitted,

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In re of Appln. 09/820,339

Version with Markings to Show Changes Made In the Claims

Claim 8 has been amended as follows:

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8 (Amended). A DNA molecule coding for the a
polypeptide-according to claim 1 capable of modulating the
autoimmune response of an individual to acetylcholine
receptor, said polypeptide being selected from the group
consisting of:
(i) a polypeptide consisting of the amino acid
sequence of SEQ ID NO:6;
(ii) a polypeptide consisting of the amino acid
sequence of SEQ ID NO:8;
(iii) a polypeptide corresponding to amino acid
residues 1-121 of SEQ ID NO:2;
(iv) a polypeptide corresponding to amino acid
residues 1-146 of SEQ ID NO:6;
(v) a polypeptide corresponding to amino acid
residues 122-210 of SEQ ID NO:2;
(vi) a polypeptide as in (i) to (v) or the
polypeptide $H\alpha 1-210$ of SEQ ID NO:2 in which one or more amino
acid residues have been added, deleted or substituted by other
amino acid residues in a manner that the resulting polypeptide
is capable of suppressing experimental myasthenia gravis in
animal models;

(vii) a fragment of a polypeptide as in (i) to (vi),
which fragment is capable of suppressing experimental
myasthenia gravis in animal models;
(viii) a polypeptide comprising two or more
fragments as in (vii) fused together with or without a spacer;
(ix) a polypeptide, or a fragment as defined in (i)-
(viii), or the polypeptide $H\alpha 1-210$ of SEQ ID NO:2, fused to an
additional polypeptide at its N- and/or C-termini; and
(x) soluble forms, denatured forms, chemical
derivatives and salts of a polypeptide or a fragment as
defined in (i)-(ix).